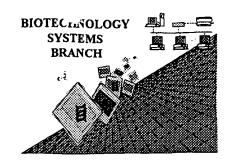
RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	09/899,634	
Source:	OIPE	· \
Date Processed by STIC:	7/24/2001	

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09/899,634	
ATTN: NEW RULES CASES	: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SO	FTWARE
1Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5Variable Length	Sequence(s)contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.	
10 J Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence 1 do not combine response	
Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
Patentin 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

AMC/MH - Biotechnology Systems Branch - 08/21/2001

OIPE

DATE: 07/24/2001

TIME: 10:14:58

Output Set: N:\CRF3\07242001\1899634.raw Corrected Diskette Needed 3 <110> APPLICANT: Thomas Buehler, Reto Andreas Gadient, Reinhard Korn, Rao Movva 4 <120> TITLE OF INVENTION: pCAR and its uses 6 <130> FILE REFERENCE: 4-31499A 8 <140> CURRENT APPLICATION NUMBER: US/09/899,634 8 <141> CURRENT FILING DATE: 2001-07-05 8 <160> NUMBER OF SEQ ID NOS: 4 10 <170> SOFTWARE: PatentIn version 3.0 12 <210> SEQ ID NO: 1 13 <211> LENGTH: 4286) invalid-sel Len 10 on Eva Summany Sheet 14 <212> TYPE: DNA C--> 15 <213> ORGANISM: (Artificial/Unknown 17 <220> FEATURE: 18 <221> NAME/KEY: CDS 19 <222> LOCATION: (3229)..(4014) 20 <223> OTHER INFORMATION: delta pCAR gene 23 <400> SEQUENCE: 1 24 cggtgcgggc ctcttcgcta ttacgccagc tggcgaaagg gggatgtgct gcaaggcgat 60 26 taagttgggt aacgccaggg ttttcccagt cacgacgttg taaaacgacg gccagtgcca 120 28 agttgggate tttgcattgg cecaeggete teaggatggg gatgeteece tteageacee 180 30 ggttcccctt ggaaactgat ggtcctggct ctgtggcatg gcagtggcac tgtgaggagc 240 32 ccctaccage agcacacagt gggtttggca ctgccacget ceggatgceg egetetgate 300 34 caaccccata atcaagggaa cccgaattgc cccatcattg cccccaccac ccccatcctg 360 36 cogggecete acaccecacy etgeettyty ytgacattee ecageceaaa eccacyyett 420 38 catggetace geggggeatt teceattgee geceeattat eagetetgea caeeteeege 480 40 tgtacccatg cetegtgget gecettettt gaegtataat ettetaatta atacceggee 540 42 ttgtcaaagt ggagcacaaa cgttaattaa ttccccaqca ggcaggtaat taacagtqtq 600 44 actccctttt tgctgcgagt ggggctgata cagagagatg tggcactatg gagcccacgg 660 46 ggtcctggca ctgggtgccc acggaggtcc ccatgtgctg cagtgtcacc gcctccgagg 720 48 tgacagtatt gtccctgcgg tgtccctgca gctcagctct gtccacaggg ccacctccag 780 50 tttggagggg acacaatgca gccccgatgc aacccatcct cgcagcatcc cagggacaaa 840 52 gaccccactg caagaccgca cacagggctg ggtcccgctc ccctaatatc tacagtgctt 900 54 ttgcatggcc ccttaatcaa tgcagttaat cagcatgcgc tcatgcaccg ctctggagct 960 1020 56 gcaaagcccc tcgcagcgct gctcaccaac accgcgcacc gccccggccc agcctgcagc 58 acqcqctqca aacaqqaaaq aaacaaaata ttqcccaaat qtaqqcaaaq qcattcqqct 1080 60 gccttgacct ccgccgggcc gggccctgcc tgactcagct ccttactcag cgctcgcttc 1140 62 ctccctccgq ctqccaccqc cqcaqcqcac accctqacaa aqaqtqqccc ttaacqqqct 1200 64 ctgaggtgca cccagcagtg cactcagcag tccaagggcc ggcctggagg tttgcaccgc 1260 66 tacgtgctga cattagcatt gaacttggcc ctgggtagtg ctgcaggccg ggcggggtgg 1320 1380 68 gtgtagagag tgcagcgcgc gttgcacccg gtgccccttc ccctcccttg catcccagca 70 ggctgcaccc cagcaccagg cccgtgcatg catgctcctg gtgttattgc agcctggtgc 1440 72 atgcatgcgt cttagtggtg cagcgctgtg catgcatcct ccttggtgtg tagcagctta 1500 74 gtgcatgcat acccctcggt gttattgctg ctctgtgcac gcacgctcat tgtatcactt 1560 76 catcccagtg catgcactca cactggagcg attgctgctc ggtgcacgca cactcattgt 1620 78 atcacgtcag ctcagtggct gcacgcacac cggtgttatt gctgctcggt gcqtqcatgc 1680 80 acatcagtgt cgctgcagct cagtgcatgc acgctcattg cccatcgcta tccctgcctc 1740 1800 82 teetgetgge geteeeeggg aggtgaette aaggggaeeg caggaeeaee tegggggtgg 1860 84 ggggagget geacaegegg acceegetee eecteeceaa caaageactg tggaateaaa

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/899,634

RAW SEQUENCE LISTING DATE: 07/24/2001 PATENT APPLICATION: US/09/899,634 TIME: 10:14:58

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	Leu	-					_	_	_		-	-	-			_	3333
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	Pro																3423
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	tac																3525
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	tca																3573
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/899,634

DATE: 07/24/2001 TIME: 10:14:58

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Input Set: A:\Backup of SEQ IDs of application 4 31499A.wbk

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors. RAW SEQUENCE LISTING DATE: 07/24/2001 PATENT APPLICATION: US/09/899,634 TIME: 10:14:58

Input Set: A:\Backup of SEQ IDs of application 4_31499A.wbk
Output Set: N:\CRF3\07242001\1899634.raw

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PATENT APPLICATION: US/09/899,634

DATE: 07/24/2001 TIME: 10:14:58

Input Set : A:\Backup of SEQ IDs of application 4_31499A.wbk
Output Set: N:\CRF3\07242001\I899634.raw

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105																		33	36
326 Cac gat att ggc aca tat cag tgc aaa gtg aaa aag gct cct ggt gtt 384		пэр	пси	цуз		Gry	лэр	Ата	261		ASII	val	1111	ASII		GIII	ьеи		
Ser Asp Ile Gly Thr Tyr Gln Cys Lys Val Lys Lys Ala Pro Gly Val 28		tca	ast	att		202	tat	C = C	taa		at a	222	224	aat		~~+	~++	2.0	2.4
115 120 125 330 341 348	320	Sor	Jan	Tlo	Clv	Thr	Tur	Cln	Cva	T	y cy	T	aay T	yct.	Dwa	ggt	guu	. 36	34
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332 130																		4.5	32
334 aga tgt tat gtt gat gga tca gga gaa gaa att gga aat gac ttt aaa cta 335 Arg Cys Tyr Val Asp Gly Ser Glu Glu Ile Gly Asn Asp Phe Lys Leu 336 145		GTA		пуз	пλэ	TTE	GIII		THIT	val	ьец	ьеu	-	PLO	ser	СТУ	LIII		
335 Arg Cys Tyr Val Asp Gly Ser Glu Glu Ile Gly Asn Asp Phe Lys Leu 160 160 138 aaa tgt gaa cca aaa gaa ggt tca ctc cca tta cta tat gaa tgg cag 528 339 Lys Cys Glu Pro Lys Glu Gly Ser Leu Pro Leu Leu Tyr Glu Typ Glu Typ Gla 170 175 175 175 175 175 175 175 175 175 175		242		tat	a++	a a t	~~~		~~~	~~~	a++	~~~		~~~	+++	222	a+ a	4.0	
336 145																		4 0	5 U.
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330			tat	M22	cca	222		aat	+ 0 2	at a	222		at a	+ - +	~~~	+~~	-	E 7	١.
340																		52	28
342 aaa ttg tcc ser aat tca cag aag ctg ccc acc ttg tgg tta gca gaa atg law		пуз	Суз	Giu	110		GIU	дту	Ser	ьеи		ьец	ьeu	тут	Giu		GIII		
343 Lys Leu Ser Asn Ser Gln Lys Leu Pro Thr Leu Trp Leu Ala Glu Met 180 185		222	tta	tcc	aat		cad		cta	CCC		++~	taa	++-	aa.		2+~	5 7	76
344 180 185 190 624 346 act tca cct gtt ata tct gta aaa aat gcc tct act gaa tac tct ggg 348 624 347 Thr Ser Pro Val Ile Ser Val Lys Asn Ala Ser Thr Glu Tyr Ser Gly 205 350 aca tac agc tgt acc gtg aaa aac aga gg gg gg tct gat cag tgc ctg 351 Thr Tyr Ser Cys Thr Val Lys Asn Arg Val Gly Ser Asp Gln Cys Leu 215 672																		57	0
346 act tca cct gtt ata tct gta aaa aat gcc tct act gaa tac tct ggg 624 347 Thr Ser Pro Val Ile Ser Val Lys Asn Ala Ser Thr Glu Tyr Ser Gly 200 205 348 195 200 205 205 350 aca tac agc tgt acc gtg aac aac aga gg gg ggc tct gat cag tgc ctg 672 672 351 Thr Tyr Ser Cys Thr Val Lys Asn Arg Val Gly Ser Asp Gln Cys Leu 200 205 352 210 205 20 20 354 ctt cgc ctg gat gtg gtt cct cct tca aat aga gct gga aca att gca 720 355 Leu Arg Leu Asp Val Val Pro Pro Pro Ser Asn Arg Ala Gly Thr Ile Ala 240 358 gga gct gtt ata gga gtt ttg ctt gct cat aga gg		пуз	пец	Der			GIII	цуз	neu		TIIL	ьец	пр	neu		GIU	Mec		
347 Thr Ser Pro Val Ile Ser Val Lys Asn Ala Ser Thr Glu Tyr Ser Gly 350 aca tac acc gtg aac acg gtg gtc ctc gtc ctc ctc ctc gtc gtc ctc ctc ctc gtc gtc ctc ctc ctc tca aca agc tct ctc ctc tca aca agc gtc ctc ctc tca aca agc gtc ctc ctc tca aat agc gtc gtc cta dtc cta aat agc gtc gtc cta dtc cta dtc cta aat agc cta dtc cta dtc cta aat agc cta dtc cta aat agc cta dtc cta aat agc cta		act	tca	cct		ata	tot	ata	·222		acc	tot	act	~ ~ ~		+ 0+	aaa	60	0.4
348																		02	24
350 aca tac agc tgt acc gtg aaa aac aga gtg ggc tct gat cag tgc ctg 672 351 Thr Tyr Ser Cys Thr Val Lys Asn Arg Val Gly Ser Asp Gln Cys Leu 352 210		1111	UCI		Val	116	Der	vaı		MSII	ліа	Ser	1111		тут	Ser	Gry		
351 Thr Tyr Ser Cys Thr Val Lys Asn Arg Val Gly Ser Asp Gln Cys Leu 352		aca	tac		tat	acc	ata	222		ana	ata	aac	tct		cac	+ ac	cta	67	7 2
352																		0 /	12
354 Ctt CgC Ctg gat gtg gtt Cct Cct tca aat aga gct gga aca att gca 355 Leu Arg Leu Asp Val Val Pro Pro Ser Asn Arg Ala Gly Thr Ile Ala 356 225		1111		DCI	Cyo	1111	vui		ASII	nrg	Val	ОТУ		изр	GIII	Суз	ыeu		
355 Leu Arg Leu Asp Val Val Pro Pro Ser Asn Arg Ala Gly Thr Ile Ala 356 225		ctt		cta	aat	ata	att		cct	tca	aat	ana		aaa	202	2++	ac a	7.2	20
356 225																		12	20
358 gga gct gtt ata gga gtt ttg ctt gct cta gtg ctc att ggt ctt att 359 Gly Ala Val Ile Gly Val Leu Leu Ala Leu Val Leu Ile Gly Leu Ile 360			211.9	10 u	7100	var		110	110	DCI	11011	_	711 U	O ± y	1111	110			
359 Gly Ala Val Ile Gly Val Leu Leu Ala Leu Val Leu Ile Gly Leu Ile 360			act	att	ata	gga		tta	ctt	act	cta		ctc	att	aat	ctt		76	58
360 245 250 255 362 gtg ttt tgc tgt cat aaa aag cgc aga gaa gaa aaa tac gaa aaa gaa 816 363 Val Phe Cys Cys His Lys Lys Arg Arg Glu Glu Lys Tyr Glu Lys Glu 260 265 270 366 gtg cat cat gat atc agg gaa gac gtg cct cct cct ccg aag agc aga acg acg aga acg 864 367 Val His His Asp Ile Arg Glu Asp Val Pro Pro Pro Lys Ser Arg Thr 368 275 280 285 370 tcc act gcc aga agc tac ctc ggc agc acc acc tcg tcc ctg gga tcc 285 285 371 Ser Thr Ala Arg Ser Tyr Leu Gly Ser Asn His Ser Ser Leu Gly Ser 300 300 374 atg tct cct tcc aac atg gaa ggc tat tcc aag act cag tat aac cag 960 315 320 375 Met Ser Pro Ser Asn Met Glu Gly Tyr Ser Lys Thr Gln Tyr Asn Gln 305 320 376 305 310 315 320 378 gta cca agc gaa gac ttt gaa cgc gct cct cct cag agt cca act ctc ccg 1008 379 320 335 382 ctc gct aag gta gct gcc cct aat ctc agc cgg atg gcg gtg cct 1056 383 320 335																		, ,	, ,
362 gtg ttt tgc tgt tgt cat aaa aag cgc aga gaa gaa gaa aaa tac gaa aaa gaa 816 363 Val Phe Cys Cys His Lys Lys Arg Arg Glu Glu Lys Tyr Glu Lys Glu 260 260 265 270 366 gtg cat cat gat atc agg gaa gac gtg cct cct ccg aag agc aga agg agg agg agg agg agg		011						200	БСС	1114		, u.	шоч	110	o'T A		110		
363 Val Phe Cys Cys His Lys Lys Arg Arg Glu Glu Lys Tyr Glu Lys Glu 364		ata	ttt	tac	tat		aaa	aad	cac	aσa		паа	aaa	tac	gaa		gaa	81	16
364																		0.1	. 0
366 gtg cat cat gat atc agg gaa gac gtg cct cct ccg aag agc aga acg 864 367 Val His His Asp Ile Arg Glu Asp Val Pro Pro Pro Lys Ser Arg Thr 368				0,70			-10		9		014	010	270	- 1 -		Lyo	Oxu		
367 Val His His Asp Ile Arg Glu Asp Val Pro Pro Pro Lys Ser Arg Thr 368		ata	cat	cat		atc	agg	gaa	gac		cct	cct	cca	aaσ		aga	acq	86	54
368																			
370 tcc act gcc aga agc tac ctc ggc agc aac cac tcg tcc ctg gga tcc 371 Ser Thr Ala Arg Ser Tyr Leu Gly Ser Asn His Ser Ser Leu Gly Ser 372							5								201	9			
371 Ser Thr Ala Arg Ser Tyr Leu Gly Ser Asn His Ser Ser Leu Gly Ser 372 290 295 300 374 atg tct cct tcc aac atg gaa ggc tat tcc aag act cag tat aac cag 960 375 Met Ser Pro Ser Asn Met Glu Gly Tyr Ser Lys Thr Gln Tyr Asn Gln 376 305 310 310 315 320 378 gta cca agc gaa gac ttt gaa cgc gct cct cag agt cca act ctc ccg 1008 379 Val Pro Ser Glu Asp Phe Glu Arg Ala Pro Gln Ser Pro Thr Leu Pro 380 325 335 336 335 382 ctc gct aag gta gct gcc cct aat ctc agc cgg atg gga gcg gtg cct 1056 383 Leu Ala Lys Val Ala Ala Pro Asn Leu Ser Arg Met Gly Ala Val Pro		tcc	act		aσa	agc	tac	ctc		aαc	aac	cac	tca		cta	gga	tcc	91	12
372																			_
374 atg tct cct tcc aac atg gaa ggc tat tcc aag act cag tat aac cag 960 375 Met Ser Pro Ser Asn Met Glu Gly Tyr Ser Lys Thr Gln Tyr Asn Gln 376 305 310 315 320 378 gta cca agc gaa gac ttt gaa cgc gct cct cag agt cca act ctc ccg 1008 379 Val Pro Ser Glu Asp Phe Glu Arg Ala Pro Gln Ser Pro Thr Leu Pro 380 325 335 335 382 ctc gct aag gta gct gcc cct aat ctc agc cgg atg gga gcg gtg cct 1056 383 Leu Ala Lys Val Ala Ala Pro Asn Leu Ser Arg Met Gly Ala Val Pro					5		- 1		1							1			
375 Met Ser Pro Ser Asn Met Glu Gly Tyr Ser Lys Thr Gln Tyr Asn Gln 376 305		atq		cct	tcc	aac	atq		aac	tat	tcc	aaq		caq	tat	aac	caq	96	50
376 305 310 315 320 378 gta cca agc gaa gac ttt gaa cgc gct cct cag agt cca act ctc ccg 1008 379 Val Pro Ser Glu Asp Phe Glu Arg Ala Pro Gln Ser Pro Thr Leu Pro 380 325 330 335 382 ctc gct aag gta gct gcc cct aat ctc agc cgg atg gga gcg gtg cct 1056 383 Leu Ala Lys Val Ala Ala Pro Asn Leu Ser Arg Met Gly Ala Val Pro																			
378 gta cca agc gaa gac ttt gaa cgc gct cct cag agt cca act ctc ccg 379 Val Pro Ser Glu Asp Phe Glu Arg Ala Pro Gln Ser Pro Thr Leu Pro 380 325 330 335 382 ctc gct aag gta gct gcc cct aat ctc agc cgg atg gga gcg gtg cct 383 Leu Ala Lys Val Ala Ala Pro Asn Leu Ser Arg Met Gly Ala Val Pro										4		_			-2				
379 Val Pro Ser Glu Asp Phe Glu Arg Ala Pro Gln Ser Pro Thr Leu Pro 380 325 330 335 335 382 ctc gct aag gta gct gcc cct aat ctc agc cgg atg gga gcg gtg cct 1056 383 Leu Ala Lys Val Ala Ala Pro Asn Leu Ser Arg Met Gly Ala Val Pro			cca	agc	qaa	gac	ttt	qaa	cqc	gct	cct	caq	agt	cca	act	ctc	ccq	100	8
380 325 330 335 382 ctc gct aag gta gct gcc cct aat ctc agc cgg atg gga gcg gtg cct 1056 383 Leu Ala Lys Val Ala Ala Pro Asn Leu Ser Arg Met Gly Ala Val Pro																			
382 ctc gct aag gta gct gcc cct aat ctc agc cgg atg gga gcg gtg cct 1056 383 Leu Ala Lys Val Ala Ala Pro Asn Leu Ser Arg Met Gly Ala Val Pro																			
383 Leu Ala Lys Val Ala Ala Pro Asn Leu Ser Arg Met Gly Ala Val Pro		ctc	gct	aag	gta		gcc	cct	aat	ctc	agc	cgg	atg	gga	gcg	gtg	cct	105	56
												_		-					

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/899,634

DATE: 07/24/2001 TIME: 10:14:59

Input Set : A:\Backup of SEQ IDs of application 4 31499A.wbk

Output Set: N:\CRF3\07242001\1899634.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier

L:8 M:270 C: Current Application Number differs, Replaced Current Application No

L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:15 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1

L:214 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2

L:216 M:258 W: Mandatory Feature missing, <220> FEATURE:

L:216 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

L:289 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3 L:394 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4

L:396 M:258 W: Mandatory Feature missing, <220> FEATURE:

L:396 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: